

SEQUENCE LISTING

<110> Lok, Si
Holloway, James L.

<120> Human V2 Vomeronasal Receptor

<130> 00-107

<150> 60/252,373
<151> 2000-11-21

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(657)

<400> 1
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Met Phe Glu Arg Arg Lys Glu Gln Asp Glu Gly Pro Gly Ile His Glu
1 5 10 15

ttt ctt gca ttt tta tgg gct gaa ttg ggc tct gaa gcc aaa gaa gag 96
Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu
20 25 30

aaa gaa gaa gaa cgg acc tgc cgg ttg ctg ggc aag tgt gta gat gcc 144
Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala
35 40 45

gaa aac cat tcc ctt gtt att gga gga ctg ttt cct att gac tcc agg 192
Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg
50 55 60

acc atc cca gca aat gag tct att ttg gag cca gca tca gca aaa tgt			240
Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys			
65	70	75	80
gaa ggg ttt aac ttt cag aga ttc cgc tgg atg aaa gcc atg atc cac			288
Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His			
85	90	95	
atg atc aag gag att aat aag agg aag gat att ttg ccc aac atc act			336
Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr			
100	105	110	
ctg ggc tat cag atc ttt gat acc tgt ttt acc atc tcc aaa tca gtg			384
Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val			
115	120	125	
gaa gca gtc ttg gta ttt ctt aca ggg cag gaa gaa aac agg ccc aat			432
Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn			
130	135	140	
ttt aga aac agc act gga gca ttt ccg gca gga att gtt gga gca ggt			480
Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly			
145	150	155	160
gga tca ttc tta tca gtt cct gct tca aga att cta ggg tta tat tat			528
Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr			
165	170	175	
ttg cct cag gtg ggc tat acc tct acc tgc gtg att ctt agt gac aaa			576
Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys			
180	185	190	
tac cag ttt cca tct tat ctt cgt gta ata gcc agc gat aag atc cag			624
Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln			
195	200	205	
tcg aag gct gtg gta aaa cgt atc caa cac ttt			657
Ser Lys Ala Val Val Lys Arg Ile Gln His Phe			
210	215		
<210> 2			
<211> 219			
<212> PRT			

<213> Homo sapiens

<400> 2

Met Phe Glu Arg Arg Lys Glu Gln Asp Glu Gly Pro Gly Ile His Glu
 1 5 10 15
 Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu
 20 25 30
 Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala
 35 40 45
 Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg
 50 55 60
 Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys
 65 70 75 80
 Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His
 85 90 95
 Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr
 100 105 110
 Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val
 115 120 125
 Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn
 130 135 140
 Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly
 145 150 155 160
 Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr
 165 170 175
 Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys
 180 185 190
 Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln
 195 200 205
 Ser Lys Ala Val Val Lys Arg Ile Gln His Phe
 210 215

<210> 3

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the
 amino acid sequence of SEQ ID NO:2.

<221> misc_feature

<222> 12, 15, 33, 36, 39, 54, 57, 63, 69, 75, 78, 81, 87, 111,

114, 120, 123, 126, 129, 138, 144, 156, 159, 162, 168, 171,
 174, 180, 189, 192, 195, 201, 204, 213, 219, 225, 228, 231,
 234, 246, 261, 267, 279, 312, 324, 327, 336, 339, 342

<223> n = A,T,C or G

<221> misc_feature

<222> 360, 369, 375, 381, 384, 390, 393, 396, 399, 405, 408, 411,
 426, 429, 438, 444, 447, 450, 453, 459, 462, 465, 471, 474,
 477, 480, 483, 486, 492, 495, 498, 501, 504, 507, 510, 516,
 519, 522, 531, 534, 540, 543, 549, 552, 555, 561, 567

<223> n = A,T,C or G

<221> misc_feature

<222> 570, 588, 591, 597, 600, 603, 609, 612, 627, 633, 636, 639,
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<223> n = A,T,C or G

<400> 3

atgttygarm gnmgnaarga rcargaygar ggnccngna thcaygartt yytngcntt 60
 ytnntggcng arytnngnws ngargcnaar gargarraarg argargarmg nacntgymgn 120
 ytnytnngna artgygtnga ygcngaraay caywsnytng tnathggngg nytnnttyccn 180
 athgaywsnm gnacnathcc ncnaaygar wsnathtyng arccngcnws ncnaartgy 240
 garginntya ayttycarmg ntymgntgg atgaargcna tgathcayat gathaargar 300
 athaayaarm gnaargayat hytnccnaay athacnytng gntaycarat httygayacn 360
 tgyttyacna thwsnaarws ngtngargcn gtnytnntnt tyytnacngg ncargargar 420
 aaymgncnna ayttymgnna ywsnacnggn gcnttyccng cnggnathgt ngnngcnggn 480
 ggnwsnttayy tnwsngtncc ncwsnmgn athytnngny tntaytayyt nccncargtn 540
 ggntayacnw snacntgygt nathytnwsn gayaartayc arttycnws ntayytnmgn 600
 gtnathgcnw sngayaarat hcarwsnaar gcngtngtna armgnathca rcaytta 657

<210> 4

<211> 1140

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1140)

<400> 4

ctt ccc cat tca gtg tgt act gat gtg tgt cct cct ggg act gga agg 48
 Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Gly Arg

1

5

10

15

gga ttc gtt cag agg gaa cca ata tgc tgc ttt gac tcc atc cca tgt			96
Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys			
20	25	30	
gct gat gga cac gtg tca cgg aaa cca ggt gaa agg gag tgt gaa caa			144
Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln			
35	40	45	
tgt ggt gaa gac tat tgg tca aat gca caa aag agc gag tgt gtg ctg			192
Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu			
50	55	60	
aaa gag gtg gaa tac ctt gct tat gat gag gcc ctg gga ttc aca ctt			240
Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu			
65	70	75	80
gtc att ctt tct gtc ttt ggg gca ttt gtg gtc ttg gca gtc aca gct			288
Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala			
85	90	95	
gtg tat gtg ata cac agg cac act ccc ctg gtg aac gcc agt gac tgg			336
Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp			
100	105	110	
cag ctg ggc ttt ctc att cag gtt tct ctg atc atc atg ctg ctg tcg			384
Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser			
115	120	125	
tcc atg ctt ttc att gac aag cca cac aac tgg tcc tgc atg gct ggc			432
Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly			
130	135	140	
cag gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct tgc ctt ctt			480
Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu			
145	150	155	160
gga aag act agt tca ctg ttt tta gcc tac aga att tcc aaa tcc aaa			528
Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys			
165	170	175	
act caa ctt aca tcc atg cac ccc ctt tat cgg aaa atc att gtg cta			576

Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu			
180	185	190	624
atc tct gtt cta gcg gag att ggc ata tgt aca gcc tac ttg ata ttg			
Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu			
195	200	205	
gaa cct ccc atg gta tac aag aac atg gaa tct caa aat aca aag atc			672
Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile			
210	215	220	
att ctg gga tgc aat gaa att tcc ata gag ttt ttg tac tcg atg ttt			720
Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe			
225	230	235	240
gga att gat gcc ttc tta gcc ttg cta tgc ttt ctt aca act ttt gtg			768
Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val			
245	250	255	
gct cgc cag tta cca gat aat tac tat gaa gga aaa tgc atc acc ttt			816
Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe			
260	265	270	
ggg atg ctt gtc ttt ttc atc att tgg atg tct ttt gtc cct gtt tat			864
Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr			
275	280	285	
ttg agc acc aaa ggc aag ttc aaa atg gct gtg gaa ata ttt gca atc			912
Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile			
290	295	300	
ttg gca tcc agc cat ggc ttg ttg ggt tgt ata ttt gct cct aag tgc			960
Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys			
305	310	315	320
ctc att att ttg ctg agg cca gag agg aac acc agt gaa att gtt tgt			1008
Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys			
325	330	335	
gga aga gtc tcc acc aca gat aat tgc atc caa ctg acc tca gct ttt			1056
Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr Ser Ala Phe			
340	345	350	

gtg agc agt gag ctt aac aat acc aca gtg tca act gtt ctg gat gac 1104
 Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val Leu Asp Asp
 355 360 365

aga gtt ttg att tac atg tgt cct ttg aag ctg caa 1140
 Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln
 370 375 380

<210> 5
 <211> 380
 <212> PRT
 <213> Homo sapiens

<400> 5
 Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Gly Arg
 1 5 10 15
 Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys
 20 25 30
 Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln
 35 40 45
 Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu
 50 55 60
 Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu
 65 70 75 80
 Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala
 85 90 95
 Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp
 100 105 110
 Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser
 115 120 125
 Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly
 130 135 140
 Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu
 145 150 155 160
 Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys
 165 170 175
 Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu
 180 185 190
 Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu
 195 200 205
 Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile
 210 215 220

Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe
 225 230 235 240
 Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val
 245 250 255
 Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe
 260 265 270
 Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr
 275 280 285
 Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile
 290 295 300
 Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys
 305 310 315 320
 Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys
 325 330 335
 Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr Ser Ala Phe
 340 345 350
 Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val Leu Asp Asp
 355 360 365
 Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln
 370 375 380

<210> 6

<211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the
 amino acid sequence of SEQ ID NO:5.

<221> misc_feature

<222> 3, 6, 12, 15, 21, 27, 33, 36, 39, 42, 45, 48, 51, 57, 63,
 69, 87, 93, 99, 105, 111, 114, 117, 123, 126, 132, 150,
 165, 171, 180, 189, 192, 201, 210, 213, 225, 228, 231, 237,
 240, 243, 249, 252, 255, 261, 264, 270, 273, 276, 279, 282
 <223> n = A,T,C or G

<221> misc_feature

<222> 285, 288, 291, 297, 306, 312, 315, 318, 321, 327, 330, 342,
 345, 351, 360, 363, 366, 378, 381, 384, 387, 393, 408, 420,
 429, 432, 438, 441, 444, 447, 450, 453, 459, 462, 468, 471,
 477, 480, 483, 489, 492, 495, 498, 504, 507, 513, 519
 <223> n = A,T,C or G

<221> misc_feature

<222> 525, 531, 537, 540, 543, 552, 555, 561, 573, 576, 582, 585, 588, 591, 600, 609, 612, 618, 624, 630, 633, 639, 657, 666, 678, 681, 696, 708, 714, 723, 732, 738, 741, 744, 747, 756, 759, 762, 768, 771, 774, 780, 783, 801, 813, 819, 825

<223> n = A,T,C or G

<221> misc_feature

<222> 828, 849, 855, 858, 861, 867, 870, 873, 879, 894, 897, 909, 915, 918, 921, 924, 930, 933, 936, 939, 951, 954, 963, 972, 975, 978, 981, 987, 993, 996, 1005, 1011, 1014, 1017, 1020, 1023, 1026, 1044, 1047, 1050, 1053, 1059, 1062, 1065

<223> n = A,T,C or G

<221> misc_feature

<222> 1071, 1080, 1083, 1086, 1089, 1092, 1095, 1098, 1107, 1110, 1113, 1128, 1131, 1137

<223> n = A,T,C or G

<400> 6

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 ccngngarm gngartgyga rcartgyggn gargaytayt ggwsnaaygc ncaraarwsn 180
 gartgygtny tnaargargt ngartayytn gcntaygayg argcnytngg nttyacnytn 240
 gtnathytnw sngtnttygg ncnttygtn gtnytnccngt tnacngcngt ntaygtnath 300
 caymgnccaya cnccnytngt naaygcnwsn gaytggcary tngnttyyt nathcargtn 360
 wsnytnatha thatgytnyt nwsnwsnatg ytnnttyathg ayaarccnca yaaytggwsn 420
 tgyatggcng gncargtnac nyngcnytn ggnnttysn tntgyytnws ntgyytnytn 480
 ggnaaracnw snwsnytntt yytngcntay mgnathwsna arwsnaarac ncarytnacn 540
 wsnatgcayc cnytntaymg naarathath gtnytnathw sngtntyngc ngarathggn 600
 athtgyacng cntayytnat hytngarccn ccnatggtnt ayaaraayat ggarwsncar 660
 aayacnaara thathytngg ntgyaaygar athwsnathg arttyytna ywsnatgtty 720
 ggnathgayg cntyytngc nytnytnyty tyytnacna cntyytngc nmgncarytn 780
 ccngayaayt aytaygargg naartgyath acnttyggna tgytngtntt yttyathath 840
 tggatgwsnt tygtnccngt ntayytnwsn acnaarggna arttyaarat ggcngtngar 900
 athtgycna thytngcnws nwsncayggn ytnytnyngt gyathttygc nccnaartgy 960
 ytnathathy tnytnmgncc ngarmgnaay acnwsngara thgtntgygg nmgngtnwsn 1020
 acnacngaya aytgyathca rytnacnwsn gcnttygtnw snwsngaryt naayaayacn 1080
 acngtnwsna cngtntyngna ygaymgngt ytnathtaya tgtgycnyt naarytnca 1140

<210> 7

<211> 2781

<212> DNA

<213> Artificial Sequence

<220>

<223> Chimeric receptor.

<221> CDS

<222> (1)...(2781)

<400> 7

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Met	Phe	Glu	Arg	Arg	Lys	Glu	Gln	Asp	Glu	Gly	Pro	Gly	Ile	His	Glu	
1	5							10					15			

ttt	ctt	gca	ttt	tta	tgg	gct	gaa	ttg	ggc	tct	gaa	gcc	aaa	gaa	gag	96
Phe	Leu	Ala	Phe	Leu	Trp	Ala	Glu	Leu	Gly	Ser	Glu	Ala	Lys	Glu	Glu	
20	25												30			

aaa	gaa	gaa	gaa	cgg	acc	tgc	cgg	ttg	ctg	ggc	aag	tgt	gta	gat	gcc	144
Lys	Glu	Glu	Arg	Thr	Cys	Arg	Leu	Leu	Gly	Lys	Cys	Val	Asp	Ala		
35	40											45				

gaa	aac	cat	tcc	ctt	gtt	att	gga	gga	ctg	ttt	cct	att	gac	tcc	agg	192
Glu	Asn	His	Ser	Leu	Val	Ile	Gly	Gly	Leu	Phe	Pro	Ile	Asp	Ser	Arg	
50	55											60				

acc	atc	cca	gca	aat	gag	tct	att	ttg	gag	cca	gca	tca	gca	aaa	tgt	240
Thr	Ile	Pro	Ala	Asn	Glu	Ser	Ile	Leu	Glu	Pro	Ala	Ser	Ala	Lys	Cys	
65	70											75		80		

gaa	ggg	ttt	aac	ttt	cag	aga	ttc	cgc	tgg	atg	aaa	gcc	atg	atc	cac	288
Glu	Gly	Phe	Asn	Phe	Gln	Arg	Phe	Arg	Trp	Met	Lys	Ala	Met	Ile	His	
85	90											95				

atg	atc	aag	gag	att	aat	aag	agg	aag	gat	att	ttg	ccc	aac	atc	act	336
Met	Ile	Lys	Glu	Ile	Asn	Lys	Arg	Lys	Asp	Ile	Leu	Pro	Asn	Ile	Thr	
100	105											110				

ctg	ggc	tat	cag	atc	ttt	gat	acc	tgt	ttt	acc	atc	tcc	aaa	tca	gtg	384
Leu	Gly	Tyr	Gln	Ile	Phe	Asp	Thr	Cys	Phe	Thr	Ile	Ser	Lys	Ser	Val	
115	120											125				

gaa	gca	gtc	ttg	gta	ttt	ctt	aca	ggg	cag	gaa	gaa	aac	agg	ccc	aat	432
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Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Asn Arg Pro Asn			
130	135	140	
ttt aga aac agc act gga gca ttt ccg gca gga att gtt gga gca ggt			480
Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly			
145	150	155	160
gga tca ttc tta tca gtt cct gct tca aga att cta ggg tta tat tat			528
Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr			
165	170	175	
ttg cct cag gtg ggc tat acc tct acc tgc gtg att ctt agt gac aaa			576
Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys			
180	185	190	
tac cag ttt cca tct tat ctt cgt gta ata gcc agc gat aag atc cag			624
Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln			
195	200	205	
tcg aag gct gtg gta aaa cgt atc caa cac ttt ggt tgg gtc tgg gta			672
Ser Lys Ala Val Val Lys Arg Ile Gln His Phe Gly Trp Val Trp Val			
210	215	220	
ggt gct att gca gct gat gat tat ggg aaa tat gga gta aaa act			720
Gly Ala Ile Ala Ala Asp Asp Tyr Gly Lys Tyr Gly Val Lys Thr			
225	230	235	240
ttt aag gaa aaa atg gag agt gcc aac ctc tgt gtt gct ttc tct gaa			768
Phe Lys Glu Lys Met Glu Ser Ala Asn Leu Cys Val Ala Phe Ser Glu			
245	250	255	
acc att ccc aaa gtc tac tcc aat gag aaa atg cag aag gct gtt aag			816
Thr Ile Pro Lys Val Tyr Ser Asn Glu Lys Met Gln Lys Ala Val Lys			
260	265	270	
gca gta aag act tcc act gcc aaa gtc att gtg ctt tat act tct gac			864
Ala Val Lys Thr Ser Thr Ala Lys Val Ile Val Leu Tyr Thr Ser Asp			
275	280	285	
att gac ctc agc ctg ttt gtg ctg gaa atg att cat cat aac ata act			912
Ile Asp Leu Ser Leu Phe Val Leu Glu Met Ile His His Asn Ile Thr			
290	295	300	

gac agg aca tgg ata gcc acc gaa gcc tgg att acc tct gct ctc att			960
Asp Arg Thr Trp Ile Ala Thr Glu Ala Trp Ile Thr Ser Ala Leu Ile			
305	310	315	320
gca aag cct gag tat ttc ccc tat ttt ggt gga act att gga ttt gca			1008
Ala Lys Pro Glu Tyr Phe Pro Tyr Phe Gly Gly Thr Ile Gly Phe Ala			
325	330	335	
aca cca aga agt gtt ata cca gga cta aaa gaa ttt ctt tat gat gta			1056
Thr Pro Arg Ser Val Ile Pro Gly Leu Lys Glu Phe Leu Tyr Asp Val			
340	345	350	
cac cct aac aag gat cca aat gat gtc ttg acc att gaa ttc tgg caa			1104
His Pro Asn Lys Asp Pro Asn Asp Val Leu Thr Ile Glu Phe Trp Gln			
355	360	365	
act gct ttt aac tgt acc tgg ccc aac agc agt gtt cct tat aac gtg			1152
Thr Ala Phe Asn Cys Thr Trp Pro Asn Ser Ser Val Pro Tyr Asn Val			
370	375	380	
gat cac aga gtg aat atg act ggg aaa gaa gac aga ctg tat gac atg			1200
Asp His Arg Val Asn Met Thr Gly Lys Glu Asp Arg Leu Tyr Asp Met			
385	390	395	400
tct gat cag ctc tgc act gga gag gag aag ctg gaa gat ctg aaa aac			1248
Ser Asp Gln Leu Cys Thr Gly Glu Lys Leu Glu Asp Leu Lys Asn			
405	410	415	
acc tat ctg gat aca tca cag cta aga att aca aaa caa tgt aaa caa			1296
Thr Tyr Leu Asp Thr Ser Gln Leu Arg Ile Thr Lys Gln Cys Lys Gln			
420	425	430	
gct gta tat gct ata gct cat ggc ctg gat cat ctc agc aga tgt caa			1344
Ala Val Tyr Ala Ile Ala His Gly Leu Asp His Leu Ser Arg Cys Gln			
435	440	445	
gaa ggg cag gga cca ttt ggc tca aat cag caa tgt gca tat ata cct			1392
Glu Gly Gln Gly Pro Phe Gly Ser Asn Gln Gln Cys Ala Tyr Ile Pro			
450	455	460	
acc ttt gat ttc tgg cag cta atg tac tat atg aaa gaa att aaa ttt			1440
Thr Phe Asp Phe Trp Gln Leu Met Tyr Tyr Met Lys Glu Ile Lys Phe			
465	470	475	480

aaa tca cat gag gat aaa tgg gta att ctg gat gat aat gga gat ttg			1488
Lys Ser His Glu Asp Lys Trp Val Ile Leu Asp Asp Asn Gly Asp Leu			
485	490	495	
aaa aat gga cac tat gat gtc cta aac tgg cac tta gat gat gag gga			1536
Lys Asn Gly His Tyr Asp Val Leu Asn Trp His Leu Asp Asp Glu Gly			
500	505	510	
gaa att tcc ttt gtg aca gtt ggg aga ttt aac ttt aga tct aca aac			1584
Glu Ile Ser Phe Val Thr Val Gly Arg Phe Asn Phe Arg Ser Thr Asn			
515	520	525	
ttt gag ctt gtt att cca acg aat tct aca ata ttt tgg aac act gag			1632
Phe Glu Leu Val Ile Pro Thr Asn Ser Thr Ile Phe Trp Asn Thr Glu			
530	535	540	
tca tca agg ctt ccc cat tca gtg tgt act gat gtg tgt cct cct ggg			1680
Ser Ser Arg Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly			
545	550	555	560
act gga agg gga ttc gtt cag agg gaa cca ata tgc tgc ttt gac tcc			1728
Thr Gly Arg Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser			
565	570	575	
atc cca tgt gct gat gga cac gtg tca cgg aaa cca ggt gaa agg gag			1776
Ile Pro Cys Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu			
580	585	590	
tgt gaa caa tgt ggt gaa gac tat tgg tca aat gca caa aag agc gag			1824
Cys Glu Gln Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu			
595	600	605	
tgt gtg ctg aaa gag gtg gaa tac ctt gct tat gat gag gcc ctg gga			1872
Cys Val Leu Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly			
610	615	620	
ttc aca ctt gtc att ctt tct gtc ttt ggg gca ttt gtg gtc ttg gca			1920
Phe Thr Leu Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala			
625	630	635	640
gtc aca gct gtg tat gtg ata cac agg cac act ccc ctg gtg aac gcc			1968

Val Thr Ala Val Tyr Val Ile His His Thr Pro Leu Val Asn Ala			
645	650	655	
agt gac tgg cag ctg ggc ttt ctc att cag gtt tct ctg atc atc atg			2016
Ser Asp Trp Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met			
660	665	670	
ctg ctg tcg tcc atg ctt ttc att gac aag cca cac aac tgg tcc tgc			2064
Leu Leu Ser Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys			
675	680	685	
atg gct ggc cag gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct			2112
Met Ala Gly Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser			
690	695	700	
tgc ctt ctt gga aag act agt tca ctg ttt tta gcc tac aga att tcc			2160
Cys Leu Leu Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser			
705	710	715	720
aaa tcc aaa actcaa ctt aca tcc atg cac ccc ctt tat cgg aaa atc			2208
Lys Ser Lys Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile			
725	730	735	
att gtg cta atc tct gtt cta gcg gag att ggc ata tgt aca gcc tac			2256
Ile Val Leu Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr			
740	745	750	
ttg ata ttg gaa cct ccc atg gta tac aag aac atg gaa tct caa aat			2304
Leu Ile Leu Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn			
755	760	765	
aca aag atc att ctg gga tgc aat gaa att tcc ata gag ttt ttg tac			2352
Thr Lys Ile Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr			
770	775	780	
tcg atg ttt gga att gat gcc ttc tta gcc ttg cta tgc ttt ctt aca			2400
Ser Met Phe Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr			
785	790	795	800
act ttt gtg gct cgc cag tta cca gat aat tac tat gaa gga aaa tgc			2448
Thr Phe Val Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys			
805	810	815	

atc acc ttt ggg atg ctt gtc ttt ttc atc att tgg atg tct ttt gtc 2496
 Ile Thr Phe Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val
 820 825 830

cct gtt tat ttg agc acc aaa ggc aag ttc aaa atg gct gtg gaa ata 2544
 Pro Val Tyr Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile
 835 840 845

ttt gca atc ttg gca tcc agc cat ggc ttg ttg ggt tgt ata ttt gct 2592
 Phe Ala Ile Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala
 850 855 860

cct aag tgc ctc att att ttg ctg agg cca gag agg aac acc agt gaa 2640
 Pro Lys Cys Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu
 865 870 875 880

att gtt tgt gga aga gtc tcc acc aca gat aat tgc atc caa ctg acc 2688
 Ile Val Cys Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr
 885 890 895

tca gct ttt gtg agc agt gag ctt aac aat acc aca gtg tca act gtt 2736
 Ser Ala Phe Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val
 900 905 910

ctg gat gac aga gtt ttg att tac atg tgt cct ttg aag ctg caa 2781
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 915 920 925

<210> 8

<211> 927

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric receptor.

<400> 8

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 Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu
 20 25 30

Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala
 35 40 45
 Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg
 50 55 60
 Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys
 65 70 75 80
 Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His
 85 90 95
 Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr
 100 105 110
 Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val
 115 120 125
 Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn
 130 135 140
 Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly
 145 150 155 160
 Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr
 165 170 175
 Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys
 180 185 190
 Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln
 195 200 205
 Ser Lys Ala Val Val Lys Arg Ile Gln His Phe Gly Trp Val Trp Val
 210 215 220
 Gly Ala Ile Ala Ala Asp Asp Asp Tyr Gly Lys Tyr Gly Val Lys Thr
 225 230 235 240
 Phe Lys Glu Lys Met Glu Ser Ala Asn Leu Cys Val Ala Phe Ser Glu
 245 250 255
 Thr Ile Pro Lys Val Tyr Ser Asn Glu Lys Met Gln Lys Ala Val Lys
 260 265 270
 Ala Val Lys Thr Ser Thr Ala Lys Val Ile Val Leu Tyr Thr Ser Asp
 275 280 285
 Ile Asp Leu Ser Leu Phe Val Leu Glu Met Ile His His Asn Ile Thr
 290 295 300
 Asp Arg Thr Trp Ile Ala Thr Glu Ala Trp Ile Thr Ser Ala Leu Ile
 305 310 315 320
 Ala Lys Pro Glu Tyr Phe Pro Tyr Phe Gly Gly Thr Ile Gly Phe Ala
 325 330 335
 Thr Pro Arg Ser Val Ile Pro Gly Leu Lys Glu Phe Leu Tyr Asp Val
 340 345 350
 His Pro Asn Lys Asp Pro Asn Asp Val Leu Thr Ile Glu Phe Trp Gln
 355 360 365

Thr Ala Phe Asn Cys Thr Trp Pro Asn Ser Ser Val Pro Tyr Asn Val
 370 375 380
 Asp His Arg Val Asn Met Thr Gly Lys Glu Asp Arg Leu Tyr Asp Met
 385 390 395 400
 Ser Asp Gln Leu Cys Thr Gly Glu Glu Lys Leu Glu Asp Leu Lys Asn
 405 410 415
 Thr Tyr Leu Asp Thr Ser Gln Leu Arg Ile Thr Lys Gln Cys Lys Gln
 420 425 430
 Ala Val Tyr Ala Ile Ala His Gly Leu Asp His Leu Ser Arg Cys Gln
 435 440 445
 Glu Gly Gln Gly Pro Phe Gly Ser Asn Gln Gln Cys Ala Tyr Ile Pro
 450 455 460
 Thr Phe Asp Phe Trp Gln Leu Met Tyr Tyr Met Lys Glu Ile Lys Phe
 465 470 475 480
 Lys Ser His Glu Asp Lys Trp Val Ile Leu Asp Asp Asn Gly Asp Leu
 485 490 495
 Lys Asn Gly His Tyr Asp Val Leu Asn Trp His Leu Asp Asp Glu Gly
 500 505 510
 Glu Ile Ser Phe Val Thr Val Gly Arg Phe Asn Phe Arg Ser Thr Asn
 515 520 525
 Phe Glu Leu Val Ile Pro Thr Asn Ser Thr Ile Phe Trp Asn Thr Glu
 530 535 540
 Ser Ser Arg Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly
 545 550 555 560
 Thr Gly Arg Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser
 565 570 575
 Ile Pro Cys Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu
 580 585 590
 Cys Glu Gln Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu
 595 600 605
 Cys Val Leu Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly
 610 615 620
 Phe Thr Leu Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala
 625 630 635 640
 Val Thr Ala Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala
 645 650 655
 Ser Asp Trp Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met
 660 665 670
 Leu Leu Ser Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys
 675 680 685
 Met Ala Gly Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser
 690 695 700

Cys Leu Leu Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser
 705 710 715 720
 Lys Ser Lys Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile
 725 730 735
 Ile Val Leu Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr
 740 745 750
 Leu Ile Leu Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn
 755 760 765
 Thr Lys Ile Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr
 770 775 780
 Ser Met Phe Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr
 785 790 795 800
 Thr Phe Val Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys
 805 810 815
 Ile Thr Phe Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val
 820 825 830
 Pro Val Tyr Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile
 835 840 845
 Phe Ala Ile Leu Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala
 850 855 860
 Pro Lys Cys Leu Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu
 865 870 875 880
 Ile Val Cys Gly Arg Val Ser Thr Thr Asp Asn Cys Ile Gln Leu Thr
 885 890 895
 Ser Ala Phe Val Ser Ser Glu Leu Asn Asn Thr Thr Val Ser Thr Val
 900 905 910
 Leu Asp Asp Arg Val Leu Ile Tyr Met Cys Pro Leu Lys Leu Gln
 915 920 925

<210> 9

<211> 2781

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID:8.

<221> misc_feature

<222> (1)...(2781)

<223> n = A,T,C or G

<400> 9

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 ytnytnngna artgygtnga ycgaraay caywsnytng tnathggngg nytnnccn 180
 athgaywsnm gnacnathcc ncnaaygar wsnathtng arccngcnws ncnaartgy 240
 garginnnya ayttycarmg ntymgntgg atgaargcna tgathcayat gathaargar 300
 athaayaarm gnaargayat hytnccnaay athacnytng gntaycarat httygayan 360
 tgyttypacna thwsnaarws ntngargcn gtnytnngtnt tyytnacngg ncargargar 420
 aaymgnccna ayttymgnaa ywsnacnggn gcnttyccng cnggnathgt ngnngcnggn 480
 ggnwsnttuy tnwsngtncc ncwsmgn athytnngny ntaytayyt nccncargtn 540
 gntayacnw snacntgyt nathytnwsn gayaartayc arttycnws ntayytnmgn 600
 gtnathgcw sngayaarat hcarwsnaar gcngtngtna armgnathca rcayttypgn 660
 tgggtntggg tnngngcnat hcngcngay gaygatyay gnaartaygg ntynaaracn 720
 ttyaargara aratggarws ncnaayytn tgytngcnt tywsngarac nathccnaar 780
 gtntaywsna aygaraarat gcaraargcn gtnaargcng tnaaracnws nacngcnaar 840
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 cayaayatha cngaymgnac ntggathgcn acngargcnt ggathacnws ncnytnath 960
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 tggwsnaayg cncaraarws ngartgytng ytnaargarg tngartayyt ncnytnayg 1860
 garginnnya gnttyacnyt ntynaaytng wsngtnttng gngcnttngt ntaytngcn 1920
 gtnacngcng ntaygtnat hcaymgnay acnccnytng tnaaygcnaa ngaytggcar 1980
 ytnytnayt tnaaytngt nwsnytnath athatgytny twnsnwsnat gytnttayth 2040
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 acnttaytng cnmgncaryt nccngayaay taytaygarg gnaartgyat hacnttnggn 2460
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aarttyaara tggcngtnga rathttygcn athytngcnw snwsncaygg nytnytnngn 2580
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athgtntgyg gnmgngtnws nacnacngay aaytgyathc arytnacnws ngcnttygtn 2700
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<210> 10

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker.

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